

INPUT SET: S18376.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

3 (1) General Information:
4
5 (i) APPLICANT: RUEGER, David C.
6 TUCKER, Marjorie M.
7
8 (ii) TITLE OF INVENTION: IMPROVED OSTEOGENIC DEVICES AND METHODS
9 OF USE THEREOF FOR REPAIR OF ENDOCHONDRAL BONE AND
10 OSTEOCHONDRAL DEFECTS
11
12 (iii) NUMBER OF SEQUENCES: 9
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: CREATIVE BIOMOLECULES, INC
16 (B) STREET: 45 SOUTH STREET
17 (C) CITY: HOPKINTON
18 (D) STATE: MA
19 (E) COUNTRY: USA
20 (F) ZIP: 01748
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER:
30 (B) FILING DATE:
31 (C) CLASSIFICATION:
32
33 (viii) ATTORNEY/AGENT INFORMATION:
34 (A) NAME: VITO, CHRISTINE C
35 (B) REGISTRATION NUMBER: 39,061
36 (C) REFERENCE/DOCKET NUMBER: CRP-137
37
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: (617) 248-7000
40 (B) TELEFAX: (617) 248-7100
41
42
43 (2) INFORMATION FOR SEQ ID NO:1:
44
45 (i) SEQUENCE CHARACTERISTICS:
46 (A) LENGTH: 1822 base pairs

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PATENT APPLICATION US/08/822,186

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47      (B) TYPE: nucleic acid
48      (C) STRANDEDNESS: single
49      (D) TOPOLOGY: linear
50
51      (ii) MOLECULE TYPE: cDNA
52
53      (vi) ORIGINAL SOURCE:
54          (A) ORGANISM: HOMO SAPIENS
55          (F) TISSUE TYPE: HIPPOCAMPUS
56
57      (ix) FEATURE:
58          (A) NAME/KEY: CDS
59          (B) LOCATION: 49..1341
60          (C) IDENTIFICATION METHOD: experimental
61          (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
62 /product= "OP1"
63 /evidence= EXPERIMENTAL
64 /standard_name= "OP1"
65
66
67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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69 GGTGCGGGCC CGGAGCCCGG AGCCCCGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG      57
70                                         Met His Val
71                                         1
72
73 CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA      105
74 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
75      5             10            15
76
77 CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC      153
78 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
79      20            25            30            35
80
81 GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG      201
82 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
83      40            45            50
84
85 CCG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GCC TTG CCC CAC CGC      249
86 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
87      55            60            65
88
89 CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG      297
90 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
91      70            75            80
92
93 CTC GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC      345
94 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Pro Gly
95      85            90            95
96
97 GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC      393
98 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
99      100           105           110           115

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100	CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC	441
101	Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp	
102	120 125 130	
103		
104		
105	ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC	489
106	Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe	
107	135 140 145	
108		
109	CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC	537
110	His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile	
111	150 155 160	
112		
113	CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC	585
114	Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
115	165 170 175	
116		
117	TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT	633
118	Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr	
119	180 185 190 195	
120		
121	CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC	681
122	Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu	
123	200 205 210	
124		
125	GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC	729
126	Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp	
127	215 220 225	
128		
129	ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG	777
130	Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu	
131	230 235 240	
132		
133	GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC	825
134	Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro	
135	245 250 255	
136		
137	AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC	873
138	Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro	
139	260 265 270 275	
140		
141	TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC	921
142	Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile	
143	280 285 290	
144		
145	CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC	969
146	Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro	
147	295 300 305	
148		
149	AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC	1017
150	Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser	
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152		

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153	AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC	1065
154	Ser Asp Gln Arg Gln Ala Cys Lys His Glu Leu Tyr Val Ser Phe	
155	325 330 335	
156		
157	CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC	1113
158	Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala	
159	340 345 350 355	
160		
161	GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG	1161
162	Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met	
163	360 365 370	
164		
165	AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC	1209
166	Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn	
167	375 380 385	
168		
169	CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC	1257
170	Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala	
171	390 395 400	
172		
173	ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA	1305
174	Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys	
175	405 410 415	
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177	TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC	1351
178	Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His	
179	420 425 430	
180		
181	GAGAATTCAAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG	1411
182		
183	GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCCTC CCTATCCCA ACTTTAAAGG	1471
184		
185	TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTG ATCAGTTTT CAGTGGCAGC	1531
186		
187	ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAAACAC	1591
188		
189	GCATAAAGAA AAATGGCCGG GCCAGGTCAAT TGGCTGGAA GTCTCAGCCA TGCACGGACT	1651
190		
191	CGTTTCCAGA GGTAAATTATG AGCCCTTACCC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG	1711
192		
193	GGCGTGGCAA GGGGTGGCA CATTGGTGTG TGTGCGAAAG GAAAATTGAC CCGGAAGTTC	1771
194		
195	CTGTAATAAA TGTCAACATA AAACGAATGA ATGAAAAAAA AAAAAAAA A	1822
196		
197		
198	(2) INFORMATION FOR SEQ ID NO:2:	
199		
200	(i) SEQUENCE CHARACTERISTICS:	
201	(A) LENGTH: 431 amino acids	
202	(B) TYPE: amino acid	
203	(D) TOPOLOGY: linear	
204		
205	(ii) MOLECULE TYPE: protein	

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206
207 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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210 1 5 10 15
211
212 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
213 20 25 30
214
215 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
216 35 40 45
217
218 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
219 50 55 60
220
221 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
222 65 70 75 80
223
224 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
225 85 90 95
226
227 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
228 100 105 110
229
230 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
231 115 120 125
232
233 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
234 130 135 140
235
236 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
237 145 150 155 160
238
239 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
240 165 170 175
241
242 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
243 180 185 190
244
245 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
246 195 200 205
247
248 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
249 210 215 220
250
251 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
252 225 230 235 240
253
254 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
255 245 250 255
256
257 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
258 260 265 270

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**SEQUENCE VERIFICATION REPORT
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